

## IN THE SPECIFICATION:

On page 1, please amend the "Cross Reference to Related Applications" paragraph (lines 3-4) as follows:

This application is a continuation of U.S. Application Serial No. 10/056,253, filed January 24, 2002, now abandoned, which is a continuation of U.S. Application Serial No. 09/443,795, filed November 19, 1999, now U.S. Patent 6,383,780, both of which are hereby incorporated herein by reference in their entirety.

On page 4, please amend the paragraph beginning at line 22 as follows:

Aminopeptidase B is an exopeptidase that removes arginine and/or lysine from various amino terminal peptide substrates. This enzyme is structurally related to leukotriene A<sub>4</sub> hydrolase. The activity of aminopeptidase B is dependent upon Zn<sup>2+</sup>. With respect to primary structure, the enzyme isolated from rat testis exhibits an amino terminal potential signal peptide and a Zn<sup>2+</sup> binding consensus sequence (HEXXHX<sub>18</sub>E) (SEQ ID NO:8). In view of the fact that the enzyme contains this consensus sequence, the enzyme can be classified as a M1 family metallopeptidase.

On page 9, please amend the paragraph beginning at line 12 as follows:

**Figure 4** shows an analysis of the aminopeptidase open reading frame for amino acids corresponding to specific functional sites. A cAMP and cGMP-dependent protein kinase phosphorylation site is found from about amino acids 356-359 with the actual modified residue being the last amino acid. A protein kinase C phosphorylation site is found from about amino acids 141-143 and 374-376 with the actual modified residue being the first amino acid. Casein kinase II phosphorylation sites are found from about amino acids 208-211, 318-321, 368-371, 386-389, 408-411, 412-415 and 496-499 with the actual modified residue being the first amino acid. N-myristoylation sites are found from about amino acids 9-14, 58-63, 119-124, 333-338, 364-369, and 614-619 with the actual modified residue being the first amino acid. An amidation site is found from about amino acids 159-162. A eucaryotic putative RNA-binding region RNP-1 signature is found from about amino acids 416-423. The protein also contains a zinc binding

region signature found in neutral zinc metallopeptidases at about amino acids 322-331. This last site also corresponds to the consensus sequence HEXXHX<sub>18</sub>E (SEQ ID NO:8) reported in Foulon *et al.* In addition, a putative nuclear localization site (KKK) (SEQ ID NO:4) occurs at amino acids 161-163.